Figure 1A Her gulin-like Factor

1	CTCTTCTTCCTCCGCTACCACCACCACACAGAAACTAGCACCAGCCCCAAATTTCA	60
. 1	S S S S A T T T P E T S T S P K F H	20
٠.		
63	ma oca coa cia mammoca ca ca a occamo coa com ommos a a coomoco coa ca a ca a coa com	100
	TACGACGACATATTCCACAGAGCGATCCGAGCACTTCAAACCCTGCCGAGACAAGGACCT T T T Y S <u>T E R S E H F K P C R D K D L</u>	120 40
. 21	1 1 1 1 5 <u>1 E R 3 E R F R F C R D R D L</u>	40
121	TGCATACTGTCTCAATGATGGCGAGTGCTTTGTGATCGAAACCCTGACCGGATCCCATAA	180
41	AYCLNDGECFVIETLTGSHK	60
181	ACACTGTCGGTGCAAAGAAGGCTACCAAGGAGTCCGTTGTGATCAATTTCTGCCGAAAAC	240
61	H C R C K E G Y O G V R C D O F L P K T	80
٠.		
•		
241		
81	DSILSDPNHLGIEFMESEEV	100
301	TTATCAAAGGCAGGTGCTGTCAATTTCATGTATCATCTTTGGAATTGTCATCGTGGGCAT	360
	Y Q R Q V L S I S C I I F G I V I V G M	120
I		*
361	GTTCTGTGCAGCATTCTACTTCAAAAGCAAAAGGAATATTACAGCAAATTCTGTGTCTGA	420
121	FCAAFYFKSKRNITANSVSE	140
		•
421		400
	GGAAAGATGGAAGGGTCTGCCAGGAGCCCAATCTGCAACAAGACAAATAATGCCT E R W K G L P S Q E P N L Q Q D K *	480 160
***		100
•		
481	AACAATGGATTAATGATGTCTACTATTCTGCAACTTACATCTCATTTCTTACTGCAT	540
541	TGGACCAGAGAAATTTAAAACTCAAATGAACTGTAAAGTTTCCACACTGACACTGTTGGG	600
601-	CTAATAGTATTCCCATGTGCAAGGCATGCATCTTTTCTTCCCCAGAGCAATGCCTCTCAT	.660
		,,,
661	GAGAGACTAATGGTATTGCAATCAGCTGCTGATTGTTTTCTCTGTTCCCATTTTCTGGG	720
721	TGAAGGAAGAAGAGCAAAAAAGTGTGTGCTTGTGAGAGAGGGAGG	780
781	GAGGCAGGCTCAGAATGGAAGGACCACGTATCTTGGAATATTACTAAGTCAGGACTTGAG	840
		٠,
341	TGAAAAAAGACTAAAGGTAAGCAAATTATAAAAGGATTTAGGAAACGCAGTCCGGTATTG	900
901	GATATTGCTTAAAGAAAATTCCCTTATAAGTTTATACTTCCAAGACTCTGAATTGGATTA	960
961	CTGCAAACATCATTAAGTGTTTCTAATTTAATCCCATGAGAGTAATGGAATCCTTGCTCT	1020

Figure 1B Heregulin-like Factor

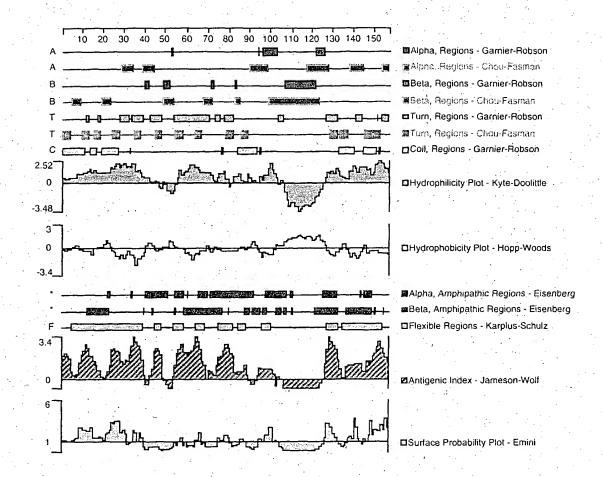
1021	GAGACATGCACTCTTACTTTTTCAGGATGATTTACCAGACTAGAACCTCCTGATTTCCCC	1080
1081	TTTTTTGTGTGTGAATGAACCCCTGATAAAATCTTGTGGCTGTAACATGCTCCTTAAA	1140
1141	ATGCTGATATGATAGATTTATTTTTAACAATAGGCTATAGATTAGCTGTTAGGAAGCAAA	1200
1201	TAGATTATTACAACAGGATTAAAGCAACTAAGAGTGCTAGAGATAAAAGTCTCCCAAATA	1260
1261	ATTGGAAAGATAAAGAAATATCTTAAAAAACAGAGCTACATCACACTGATATTGTAAAT	1320
1321	TCAAAATGGGTAATGAAGCTCAAAGCCTCCAAAGCTTGCAGCAAGTGCTGGTGAATTGCT	1380
1321	TCAAAATGGGTAATGAAGCTCCAAGCTTGCAGGAAGTGGTGGTATATGCT	1300
1381	TGGGAAGATGCAACTAGTGTAATCTTTTACCTTTGGGTCAATGTTCTGATTCTTTTGCAG	1440
1201	TOGGAAGATGCAACTAGTGTAATCTTTTACCTTTGGGTCAATGTTCTGATTCTTTTGCAG	1440
1 4 4 1	COMPANY OF A CALCULAR	1500
1441	CTTCTGCTCACAAGACTGAGCTTGCTTGATGGTATCGGGAAAGATATGAACATTTTGCGT	1500
		1560
1501	GTGCCTCCACATGCAGCCACCACAGTGTCCGTGGAAGATAGCTTTTATGAACTTCATTTA	. T200
1561	CAGAGGAGGAAATGGAGGCTCAACAAGTTTAGGAAATTATTAGGGTAGCAAAACTAGTGG	1620
		1.600
1621	GTAGCAGAGTGGGATTCAAATCCCAGTCCCTGTGATACAATAAGCCACGCTCTGTAGGGT	1680
1681	GCTACTGACTGGAGAAGCTCATTGCTAAGACCGGCCATGTGCTCCACTGACGGCACTATC	1/40
1741	TTTGTCAGAGACGTTGGAAGACAGGCAAAATTCAAGGGCATGATTCTACTGGGAAAGTTG	1800
1801	TCAGAATCAAAATGGAGTCATTTGTGTTAAAAACCCTGACAAATAGAGCCGGAGAAGGAC	1860
· · · · ·		
1861	ATGAAGGGAGCAGTCACGTAGGCAAATGCCTGATTACAAGAACTATCACAAAAGTCTGTG	1920
•.		٠.
1921	AAAACCGCAGCTTTGCATGAAGACTATTGCAGCCTTACACGCACG	1980
:		
1981	GGACATATGCCCAGCAACTTCCTGTCCACCCTTGGACTGGCTCCTCCTTTCTTGGGATCC	2040
2041	TTGCAGCCAAGGATAGTGACCTCAAATCAGTTGTGTACCTAACGTTTCCTGTCTTCCTAG	2100
2101	TGATAAAACATAGTTTCCTATATCGTGTGTATTCCCATTGCAACACTTATTTCCAAATAA	2160
•		

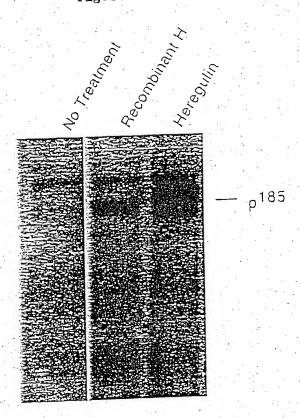
Figure 2

Heregulin-like Factor x Human Heregulin

Perc	cent Similarity: 55.782 Percent Identity: 32.653	
2	SSSSATTTTPETSTSPKFHTTTYSTERSEHFKPCRDKDLAYĆLNDGECFV	51
149	SSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFM	198
52	IETLTGSHKH.CRCKEGYQGVRCDQFLPKTDSILSDPNHLGIEFMESEEV : :	100
199	VKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEEL	243
101	YQRQVLSISCIIFGIVIVGMFCAAFYFKSKRNITANSVSEERWKGLPSQE	150
244	YOKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSER	291
151	PNLQQ 155	
 292	NNMMN 296	: '

Figure 3
Heregulin-like Factor





Amino Acid Sequences of EGF Binding Domains

14 20 31 SHFNDCPDSHTQFCFHG-TCRFLVQEDKP---ACVCHSGYVGARCEHADLLA αTGF EGF RNSDSECPLSHDGYCLHDGVCMYIEALDKY---ACNCVVGYIGERCOYRDLKW HB-EGF GKKRDPCLRKYKDFCIHG-ECKYVKELRAP---SCICHPGYGGERCHGLSLP RKKKNPCNAEFQNFCIHG-ECKYIEHLEAV---TCKCQQEYFGERCGEKSMKT Amph KGHFSRCPKQYKHYCIKG-RCRFVVAEQTP---SCVCDEGYIGARCERVDLFY Bcell neuR TSHLIKCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCOPGFTGARCTENVPMK TSHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMK Hrga1 Hrg\$1 TSHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMAS SGHARKCNETAKSYCVNGGVCYYIEGINQLS---CKCPVGYTGDRCQQFAMVN HRG-2 HLF SEHFKPCRDKDLAYCLNDGECFVIETLTGSHK-HCRCKEGYOGVRCDOFLPKT